



PCT10

RAW SEQUENCE LISTING

DATE: 06/21/2002

PATENT APPLICATION: US/10/019,633

TIME: 11:46:04

Input Set : A:\BB1386 US PCT substitute sequence listing.txt

Output Set: N:\CRF3\06212002\J019633.raw

3 <110> APPLICANT: Caspar, Timothy
 4 Falco, Saverio Carl
 5 Sakai, Hajime
 6 Weng, Zude
 7 Hu, Xu
 9 <120> TITLE OF INVENTION: PURINE METABOLISM GENES IN PLANTS
 11 <130> FILE REFERENCE: BB-1386
 13 <140> CURRENT APPLICATION NUMBER: 10/019,633
 C--> 14 <141> CURRENT FILING DATE: 2002-05-28
 16 <150> PRIOR APPLICATION NUMBER: 60/146,473
 17 <151> PRIOR FILING DATE: 1999-07-30
 19 <160> NUMBER OF SEQ ID NOS: 24
 21 <170> SOFTWARE: Microsoft Office 97
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1910
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Zea mays
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 31 gttgatggcg ttatccatgt ttatgcgat aaagattgta cggagagcat ttatcctgtg 180
 32 gctgatgcta caaccttctt cactgacttg cattatatc tccgagtaac ggctgcaggg 240
 33 aacacaagaa ctgtctgcca taatcgggtaaatcttcttg agcataagtt taaattccat 300
 34 ctgatgttaa atgcgatag ggaatttctt gccagaaga ctgccccaca tcgtgatttt 360
 35 tacaatgtca ggaaggttga cactcatgtt catcattcag catgcatgaa tcaaaaacat 420
 36 ctgttgaggt tcataaaatc caaactaaga aaagaacctg atgaggtggt cattttcaga 480
 37 gatggtactt atatgacttt aaaagagggt tttgagagct tggacttaac tgggtatgat 540
 38 ctgaatgttg atttgctaga tgtccatgca gacaaaagca catttcatcg ttttgacaaa 600
 39 ttcaatctaa aatacaatcc atgtggccaa agtaggctca gagaaatttt cctcaaaacaa 660
 40 gataatctta ttcaaggccg ttttcttgct gagttgacaa agcaagtttt ctctgacctt 720
 41 tctgctagca aatatcagat ggcagaatat aggatttcaa tctacggaag gaaacagagt 780
 42 gaatgggacc aacttgcaag ttggatagtg aacaatgaat tgcacagtgg aaatgttgct 840
 43 tggctggttc agattccacg cttatataat gtgtacaagg aaatgggtat cgttacatca 900
 44 ttccaaaatc ttcttgacaa cattttcgtt cctctttttg aggttactat tgatccagct 960
 45 tcacaccac agctccatgt cttcctgaag caggtttagt ggttgacct ggttgatgat 1020
 46 gaaagtaaac cagaaaggcg tccaacaaag cacatgcccacacctgaaca gtggaccaat 1080
 47 gtgttcaacc ctgcattttc atattatgcy tactactgct atgctaactt attcacccta 1140
 48 aacaagctgc gtgagtcaaa gggaatgacc actatcaaat tccgtccaca tgctggagag 1200
 49 gctggagatg ttgatcactt ggcagcgaca tttcttctct gtcacaacat atcacatgga 1260
 50 attaatctaa ggaagtctcc tgtgcttcag tacttgctact atcttgggtca gattgggtctg 1320
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 52 acgttcttcc aacgaggtct gaatgtctca ttatctacgg atgacccttt gcaaattcac 1440
 53 ctgacaaaag aaccattggt ggaagaatac agcattgctg cttcgctgtg gaagctcagt 1500

ENTERED

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55 ctcaaggcgc actggattgg taagaactac ttcaaaagag gacctgctgg aaatgatatt 1620
56 cacagaacca atgtaccgca catcagggtt caatttagag agatgatctg gagaaatgaa 1680
57 atgaaactag tgtactctga caatgagatc ttaataccag acgagctgga cctgtaagat 1740
58 gtccagcctc gtgtatacca gacgagttgc gttgtagctg ctatgggaat tatacttcat 1800
59 gtttttggtat gctttcctta tctatggcaa attcaacttc gaacttcaaa aaaaaaaaaa 1860
60 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1910
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63 <211> LENGTH: 578
64 <212> TYPE: PRT
65 <213> ORGANISM: Zea mays
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69 1 5 10 15
71 Cys Thr Pro Lys Pro Asn Pro Asn Pro Phe Thr Tyr Val Pro Glu Pro
72 20 25 30
74 Lys Ser Glu His Val Phe Gln Thr Val Asp Gly Val Ile His Val Tyr
75 35 40 45
77 Ala Asp Lys Asp Cys Thr Glu Ser Ile Tyr Pro Val Ala Asp Ala Thr
78 50 55 60
80 Thr Phe Phe Thr Asp Leu His Tyr Ile Leu Arg Val Thr Ala Ala Gly
81 65 70 75 80
83 Asn Thr Arg Thr Val Cys His Asn Arg Leu Asn Leu Leu Glu His Lys
84 85 90 95
86 Phe Lys Phe His Leu Met Leu Asn Ala Asp Arg Glu Phe Leu Ala Gln
87 100 105 110
89 Lys Thr Ala Pro His Arg Asp Phe Tyr Asn Val Arg Lys Val Asp Thr
90 115 120 125
92 His Val His His Ser Ala Cys Met Asn Gln Lys His Leu Leu Arg Phe
93 130 135 140
95 Ile Lys Ser Lys Leu Arg Lys Glu Pro Asp Glu Val Val Ile Phe Arg
96 145 150 155 160
98 Asp Gly Thr Tyr Met Thr Leu Lys Glu Val Phe Glu Ser Leu Asp Leu
99 165 170 175
101 Thr Gly Tyr Asp Leu Asn Val Asp Leu Leu Asp Val His Ala Asp Lys
102 180 185 190
104 Ser Thr Phe His Arg Phe Asp Lys Phe Asn Leu Lys Tyr Asn Pro Cys
105 195 200 205
107 Gly Gln Ser Arg Leu Arg Glu Ile Phe Leu Lys Gln Asp Asn Leu Ile
108 210 215 220
110 Gln Gly Arg Phe Leu Ala Glu Leu Thr Lys Gln Val Phe Ser Asp Leu
111 225 230 235 240
113 Ser Ala Ser Lys Tyr Gln Met Ala Glu Tyr Arg Ile Ser Ile Tyr Gly
114 245 250 255
116 Arg Lys Gln Ser Glu Trp Asp Gln Leu Ala Ser Trp Ile Val Asn Asn
117 260 265 270
119 Glu Leu His Ser Gly Asn Val Val Trp Leu Val Gln Ile Pro Arg Leu
120 275 280 285
122 Tyr Asn Val Tyr Lys Glu Met Gly Ile Val Thr Ser Phe Gln Asn Leu

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126 305      310      315      320
128 Ser His Pro Gln Leu His Val Phe Leu Lys Gln Val Val Gly Leu Asp
129      325      330      335
131 Leu Val Asp Asp Glu Ser Lys Pro Glu Arg Arg Pro Thr Lys His Met
132      340      345      350
134 Pro Thr Pro Glu Gln Trp Thr Asn Val Phe Asn Pro Ala Phe Ser Tyr
135      355      360      365
137 Tyr Ala Tyr Tyr Cys Tyr Ala Asn Leu Phe Thr Leu Asn Lys Leu Arg
138      370      375      380
140 Glu Ser Lys Gly Met Thr Thr Ile Lys Phe Arg Pro His Ala Gly Glu
141 385      390      395      400
143 Ala Gly Asp Val Asp His Leu Ala Ala Thr Phe Leu Leu Cys His Asn
144      405      410      415
146 Ile Ser His Gly Ile Asn Leu Arg Lys Ser Pro Val Leu Gln Tyr Leu
147      420      425      430
149 Tyr Tyr Leu Gly Gln Ile Gly Leu Ala Met Ser Pro Leu Ser Asn Asn
150      435      440      445
152 Ser Leu Phe Leu Asp Tyr His Arg Asn Pro Phe Pro Thr Phe Phe Gln
153      450      455      460
155 Arg Gly Leu Asn Val Ser Leu Ser Thr Asp Asp Pro Leu Gln Ile His
156 465      470      475      480
158 Leu Thr Lys Glu Pro Leu Val Glu Glu Tyr Ser Ile Ala Ala Ser Leu
159      485      490      495
161 Trp Lys Leu Ser Ser Cys Asp Leu Cys Glu Ile Ala Arg Asn Ser Val
162      500      505      510
164 Tyr Gln Ser Gly Phe Ser His Ala Leu Lys Ala His Trp Ile Gly Lys
165      515      520      525
167 Asn Tyr Phe Lys Arg Gly Pro Ala Gly Asn Asp Ile His Arg Thr Asn
168      530      535      540
170 Val Pro His Ile Arg Val Gln Phe Arg Glu Met Ile Trp Arg Asn Glu
171 545      550      555      560
173 Met Lys Leu Val Tyr Ser Asp Asn Glu Ile Leu Ile Pro Asp Glu Leu
174      565      570      575
176 Asp Leu
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180 <211> LENGTH: 1816
181 <212> TYPE: DNA
182 <213> ORGANISM: Oryza sativa
184 <400> SEQUENCE: 3
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186 ccgatagaga actacttgct cagaaagctg caccatcg ggacttctac aatgtcagga 120
187 aggttgatac tcatgttcat cactctgcat gcatgaatca gaagcatctg ttgagattta 180
188 tcaagtccaa gttgaggaaa gaacctgacg aggttgatgat ttttagagat ggtacctatt 240
189 tgactcttaa ggaggttttt gagagtttgg acttgactgg ttatgacctc aatgttgatc 300
190 tcttagatgt gcatgccgat aaaagtacat tccatcgctt tgacaagttc aatttgaagt 360
191 ataatccttg tggccaatcc cggctgaggg agatctttct taaacaggac aaccttattc 420
192 aaggccgatt tcttgctgaa ttgacaaaag aagtattttc tgatcttgaa gcaagtaaat 480

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Input Set : A:\BB1386 US PCT substitute sequence listing.txt

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194 tggcaagctg gatagtgaat aatgaattgt acagcgagaa tgttgtttgg ttaattcaga 600
195 ttcctcggat atacaatgta tacagggaga tgggaacaat caattctttc cagaacctcc 660
196 ttgacaatat ttttctgcct ctttttgaag taactgttga tcctgcttca catcctcagc 720
197 tccatgtttt cttgcaacag gtcgttgggc tggatttagt ggatgatgaa agcaaaccag 780
198 agagacgccc aacaaaacac atgcctacac ctgagcaatg gactaatgtt ttcaatccag 840
199 catatgcata ttatgtgtac tattgttatg ctaacttgta cacgctgaac aagcttcgtg 900
200 agtccaaggg tatgacaaca atcaaacttc gtccacactg tggggaggct ggagatattg 960
201 atcatcttgc tgcagcattt cttactttctc ataattattgc tcacgggggtt aatttaaaga 1020
202 agtccccctgt cctccagtat ctgtattacc tagctcagat tggctctgcc atgtctcctt 1080
203 tgagcaacaa ctcaatgttt attgattatc accgaaaccc tttcccaaca ttttctctaa 1140
204 gaggccttaa cgtttctcta tcaaccgatg accctttgca aattcacctg acaaaagaac 1200
205 ctttggttga agaatatagc atcgtgtgctt cgctgtggaa gctaagttca tgcgacctat 1260
206 gtgaaattgc taggaattct gtgtaccagt ctggtttctc tcataggctc aagtcacact 1320
207 ggattgggag aaactactac aaaagaggctc atgatggcaa tgacattcac cagacaaatg 1380
208 ttctcaccat caggattgaa ttccgacaca ctatttggaa agaagaaatg gagctaatac 1440
209 atctgaggaa tgttgatata ccggaagaaa ttgatagggtg aagacctggc aagaattttg 1500
210 caaaccttga agttacttgg ttgttgatga tggctctgga aggcacccca tcttcctacc 1560
211 ataaactttc caggtacaac caagaccgtg cggtttctac ttgcttgceg aagggaggag 1620
212 aaagggatct aggatgattc tacttttcga tgaatctccg tagcgtgttg cgttccctag 1680
213 tagtaggatt ttgataaaaag aaattatgtt aggactgagg ccgtaccata aaataagaaa 1740
214 gatttgagtc atggaatact ggaagttaa acataaaaaa aaaaaaaaaa aaaaaaaaaa 1800
215 aaaaaaaaaa aaaaaa 1816
217 <210> SEQ ID NO: 4
218 <211> LENGTH: 492
219 <212> TYPE: PRT
220 <213> ORGANISM: Oryza sativa
222 <400> SEQUENCE: 4
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224 1 5 10 15
226 Met Val Asn Ala Asp Arg Glu Leu Leu Ala Gln Lys Ala Ala Pro His
227 20 25 30
229 Arg Asp Phe Tyr Asn Val Arg Lys Val Asp Thr His Val His His Ser
230 35 40 45
232 Ala Cys Met Asn Gln Lys His Leu Leu Arg Phe Ile Lys Ser Lys Leu
233 50 55 60
235 Arg Lys Glu Pro Asp Glu Val Val Ile Phe Arg Asp Gly Thr Tyr Leu
236 65 70 75 80
238 Thr Leu Lys Glu Val Phe Glu Ser Leu Asp Leu Thr Gly Tyr Asp Leu
239 85 90 95
241 Asn Val Asp Leu Leu Asp Val His Ala Asp Lys Ser Thr Phe His Arg
242 100 105 110
244 Phe Asp Lys Phe Asn Leu Lys Tyr Asn Pro Cys Gly Gln Ser Arg Leu
245 115 120 125
247 Arg Glu Ile Phe Leu Lys Gln Asp Asn Leu Ile Gln Gly Arg Phe Leu
248 130 135 140
250 Ala Glu Leu Thr Lys Glu Val Phe Ser Asp Leu Glu Ala Ser Lys Tyr
251 145 150 155 160
253 Gln Met Ala Glu Tyr Arg Ile Ser Ile Tyr Gly Arg Lys Lys Ser Glu

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TIME: 11:46:04

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Output Set: N:\CRF3\06212002\J019633.raw

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259 Asn Val Val Trp Leu Ile Gln Ile Pro Arg Ile Tyr Asn Val Tyr Arg
260          195          200          205
262 Glu Met Gly Thr Ile Asn Ser Phe Gln Asn Leu Leu Asp Asn Ile Phe
263          210          215          220
265 Leu Pro Leu Phe Glu Val Thr Val Asp Pro Ala Ser His Pro Gln Leu
266 225          230          235          240
268 His Val Phe Leu Gln Gln Val Val Gly Leu Asp Leu Val Asp Asp Glu
269          245          250          255
271 Ser Lys Pro Glu Arg Arg Pro Thr Lys His Met Pro Thr Pro Glu Gln
272          260          265          270
274 Trp Thr Asn Val Phe Asn Pro Ala Tyr Ala Tyr Tyr Val Tyr Tyr Cys
275          275          280          285
277 Tyr Ala Asn Leu Tyr Thr Leu Asn Lys Leu Arg Glu Ser Lys Gly Met
278          290          295          300
280 Thr Thr Ile Lys Leu Arg Pro His Cys Gly Glu Ala Gly Asp Ile Asp
281 305          310          315          320
283 His Leu Ala Ala Ala Phe Leu Thr Ser His Asn Ile Ala His Gly Val
284          325          330          335
286 Asn Leu Lys Lys Ser Pro Val Leu Gln Tyr Leu Tyr Tyr Leu Ala Gln
287          340          345          350
289 Ile Gly Leu Ala Met Ser Pro Leu Ser Asn Asn Ser Met Phe Ile Asp
290          355          360          365
292 Tyr His Arg Asn Pro Phe Pro Thr Phe Phe Leu Arg Gly Leu Asn Val
293          370          375          380
295 Ser Leu Ser Thr Asp Asp Pro Leu Gln Ile His Leu Thr Lys Glu Pro
296 385          390          395          400
298 Leu Val Glu Glu Tyr Ser Ile Ala Ala Ser Leu Trp Lys Leu Ser Ser
299          405          410          415
301 Cys Asp Leu Cys Glu Ile Ala Arg Asn Ser Val Tyr Gln Ser Gly Phe
302          420          425          430
304 Ser His Arg Leu Lys Ser His Trp Ile Gly Arg Asn Tyr Tyr Lys Arg
305          435          440          445
307 Gly His Asp Gly Asn Asp Ile His Gln Thr Asn Val Pro His Ile Arg
308          450          455          460
310 Ile Glu Phe Arg His Thr Ile Trp Lys Glu Glu Met Glu Leu Ile His
311 465          470          475          480
313 Leu Arg Asn Val Asp Ile Pro Glu Glu Ile Asp Arg
314          485          490

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316 <210> SEQ ID NO: 5

317 <211> LENGTH: 551

318 <212> TYPE: DNA

319 <213> ORGANISM: Glycine max

321 <220> FEATURE:

322 <221> NAME/KEY: unsure

323 <222> LOCATION: (290)

324 <223> OTHER INFORMATION: n= a, t, c, or g

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/019,633

DATE: 06/21/2002
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 290,294,317,396,411,455,510,513,540
Seq#:7; N Pos. 230,377,389,439,447,465,467,474,482,492,497,509,521,530,538
Seq#:7; N Pos. 568,569,579,587,600,601,616,620,632,638,641,661
Seq#:8; Xaa Pos. 56,81,105
Seq#:9; N Pos. 412,425,433,449,471,502,518,526,538,543,546,560,563,568,570
Seq#:9; N Pos. 572,575,576,577,586,594,595,608,619,642,657,660,661,672
Seq#:11; N Pos. 475,477,526
Seq#:13; N Pos. 4,5,9,12,14,17,18,24,45,54,57,63,69,73,74,81,85,94,118,119
Seq#:13; N Pos. 122,129,130,142,165,167,168,176,179,190,202,203,214,218,230
Seq#:13; N Pos. 235,241,244,250,277,293,315,320,328,357,367,411,497
Seq#:14; Xaa Pos. 15